AMENDMENTS TO THE SPECIFICATION

Please insert paragraph [000.1], after the title and prior to paragraph [0001]. Please replace paragraphs [0029] and [0035] with the following paragraphs. Please replace the table marked as Table 1, at the end of paragraph [0078] and prior to paragraph [0079] with replacement Table 1. Replacement paragraphs 0029 and 0035 and Table 1 contain markings to show changes.

[000.1] This application claims priority to United States Provisional Application Serial No. 60/190,027, filed March 17, 20000 and is also a continuation-in-part of United States Application serial number 09/809,029 filed March 16, 2002.

[0029] Preferably, the derivatives and variants are closely related to one or more components of the naturally occurring MHC molecules, e.g. are encoded by nucleic acid molecules with more than 70%, preferably more than 80, 90 or 95% sequence identity to naturally occurring sequences or exhibit such sequence identity to the functional portions of these sequences, e.g. to naturally occurring allelic geographical or allotypic variants e.g. to sequences as described in the MGT website ~~(http://www.ebi.ac.uk/img/hla)~~ which is available on the world wide web at www.ebi.ac.uk/img/hla. Preferably said derivatives or variants exhibit the above-stated sequence identity to sequences identified in "Nomenclature for factors of the HLA system, 1998, Tissue Antigens 1999: 53, 407-446". Such derivatives or variants may be for example, as described in (http://www.ebi.ac.uk/img/hla) or Table 4. Alternatively stated, the encoded polypeptides may exhibit more than 70%, preferably more than 80, 90 or 95% sequence identity or exhibit such sequence identity to the functional portions of these sequences, e.g. to naturally occurring allelic geographical or allotypic variants e.g. to sequences as described in the IMGT website ~~(http://www.ebi.ac.uk/img/hla)~~ which is available on the world wide web at www.ebi.ac.uk/img/hla. Preferably said derivatives or variants exhibit the above-stated sequence

identity to sequences disclosed in "Nomenclature for factors of the HLA system, 1998, Tissue Antigens 1999: 53, 407-446". Such derivatives or variants may be for example, as described ~~in (http://www.ebi.ac.uk/img/hla)~~ on the world wide web at www.ebi.ac.uk/img/hla or Table 4.

[0035] Multiple alignment parameters – Matrix: PAM, Gap open penalty: 10.00, % identity for delay: 30, Penalize end gaps: on, Gap separation distance: 0, Negative matrix: no, Gap extension penalty: 0.20, Residue-specific gap penalties: on, Hydrophilic gap penalties: on, Hydrophilic residues: GPSNDQEKR (SEQ ID NO: 1). Sequence identity at a particular residue is intended to include identical residues which have simply been derivatized.

Table 1 Details of recombinant monomer/peptide combinations used

Monomer ID	**Allele**	**Peptide sequence**
A2/gag (6)	A*0201	SLYNTVATL (9) (SEQ ID NO: 2)
B7/EBV	B*0702	RPPIFIRRL (10) (SEQ ID NO: 3)
[[BB]]B8/HCV (8)	B*0801	HSKKKKDEL (11) (SEQ ID NO: 4)
A11/nef	A*1101	QVPLRPMTYK (12) (SEQ ID NO: 5)
A11/pol	A*1101	AIFQSSMTK (13) (SEQ ID NO: 6)
A11/EBV1	A*1101	IVTDFSVIK (SEQ ID NO: 7)
A11/EBV2	A*1104	AVFDRKSVIK (14) (SEQ ID NO: 8)